

In the claims:

1. (canceled)

2. (original) A double-stranded ribonucleic acid (dsRNA), consisting of first and second single RNA strands, having increased effectiveness in inhibiting the expression of a target gene by means of RNA interference, wherein the dsRNA comprises first and second double-stranded ends, wherein both double-stranded ends independently comprise a nucleotide overhang of 1 to 4 unpaired nucleotides, wherein the nucleotide overhang on at least one double-stranded end is 5'-GC-3'; wherein the terminal base pair of the first double-stranded end comprises a guanine-cytosine (G-C) base pair or the four consecutive terminal base pairs of the first double-stranded end comprises at least two G-C base pairs; wherein the terminal base pair of the second double-stranded end comprises a guanine-cytosine (G-C) base pair or the four consecutive terminal base pairs of the second double-stranded end comprises at least two G-C base pairs; excluding the following dsRNAs:

5'- CCGCUUGACUGCAGAGAGUGC-3' (SEQ ID NO: 19)
3'-UCGGCGAACUGACGUCUCUCA-5' (SEQ ID NO: 20),

5'- CAUCUUCUUAAGGACGACGGC-3' (SEQ ID NO: 21)
3'-UGGUAGAAGAAGUUCCUGCUGC-5' (SEQ ID NO: 22),

5'- GGUGGCGCUGGAUGGUAAGCCGC-3' (SEQ ID NO: 23)
3'-UACCACCGCGACCUACCAUUCGG-5' (SEQ ID NO: 24),

5'- UCCCCAGGAGGCCUGCGGGAGC-3' (SEQ ID NO: 25)
3'-GGAGGGGUCCUCCGGACGCCCU-5' (SEQ ID NO: 26),

5'- UGCAGCUUCGAAGCCUCACAGA-3' (SEQ ID NO: 27)
3'-CGACGUCGAAGCUUCGGAGUGU-5' (SEQ ID NO: 28),

5'- UGGGGAGAGAGUUCUGAGGAUU-3' (SEQ ID NO: 29)
3'-CGACCCUCUCUCAAGACUCCU-5' (SEQ ID NO: 30),

5'- ACCUCCGCAACAACUACGCGC-3' (SEQ ID NO: 31)
3'-GAUGGAGGCGUUGUUGAUGCG-5' (SEQ ID NO: 32),

5'- GUAGACCUUGCUCACUGCCUGC-3' (SEQ ID NO: 33)
3'-ACCAUCUGGAACGAUGACGGA-5' (SEQ ID NO: 34),

5'- CAUGACGGAACUAGAGACAGC-3' (SEQ ID NO: 35)
 3'-UGGUACUGCCUUGAUCUCUGU-5' (SEQ ID NO: 36),

5'- CUCUACGCUUGUACGAGGAGC-3' (SEQ ID NO: 37)
 3'-CAGAGAUGCGAACAUGCUCU-5' (SEQ ID NO: 38),

5'- CAGACUUCGGAGUACCUGCGC-3' (SEQ ID NO: 39)
 3'-UUGUCUGAAGCCUCAUGGACG-5' (SEQ ID NO: 40) and

5'- CAUCUUCUUCAAGGACGACGGC-3' (SEQ ID NO: 41)
 3'- UGGUAGAAGAAGUCCUGCUGC-5' (SEQ ID NO: 42).

Claims 3-18 (**canceled**)

19. (**original**) A method for the targeted selection of a double-stranded ribonucleic acid (dsRNA), consisting of first and second single RNA strands, having increased effectiveness in inhibiting the expression of a target gene by means of RNA interference, comprising the steps of:

(a) selecting a dsRNA comprising first and second double-stranded ends, wherein only one double-stranded end comprises a nucleotide overhang of 1 to 4 unpaired nucleotides in length;

(b) selecting a dsRNA comprising first and second double-stranded ends, wherein the unpaired nucleotide adjacent to the terminal nucleotide base pair comprises a purine base;

(c) selecting a dsRNA comprising first and second double-stranded ends, wherein the terminal base pair of the first double-stranded end comprises a guanine-cytosine (G-C) base pair or the four consecutive terminal base pairs of the first double-stranded end comprises at least two G-C base pairs; wherein the terminal base pair of the second double-stranded end comprises a guanine-cytosine (G-C) base pair or the four consecutive terminal base pairs of the second double-stranded end comprises at least two G-C base pairs; and .

(d) excluding the following dsRNAs:

5'- CAGGACCUCGCCGCGCUGCAGACC-3' (SEQ ID NO: 1)
 3'-CGGUCCUGGAGCGGCGACGUCUGG-5' (SEQ ID NO: 2),

 5'- GCCUUUGUGGAACUGUACGGCC-3' (SEQ ID NO: 3)
 3'-UACGGAAACACCUUGACAUGCCGG-5' (SEQ ID NO: 4),

 5'-CUUCUCCGCCUCACACCGCUGCAA-3' (SEQ ID NO: 5)
 3'-GAAGAGGCGGAGUGUGGCGACG-5' (SEQ ID NO: 6),

 5'- ACGGCUAGCUGUGAAAGGUCC-3' (SEQ ID NO: 13)
 3'-AGUGCCGAUCGACACUUUCCAGG-5' (SEQ ID NO: 14),

 5'- CAAGGAGCAGGGACAAGUUAC-3' (SEQ ID NO: 15)
 3'-AAGUUCCUCGUCCCUGUCAAUG-5' (SEQ ID NO: 16) and

 5'-CACGUACGCGGAAUACUUCGAAA-3' (SEQ ID NO: 17)
 3'-GUGCAUGCGCCUUAUGAAGCU-5' (SEQ ID NO: 18).

20. **(original)** A method for the targeted selection of a double-stranded ribonucleic acid (dsRNA), consisting of first and second single RNA strands, having increased effectiveness in inhibiting the expression of a target gene by means of RNA interference, comprising the steps of:

- (a) selecting a dsRNA comprising first and second double-stranded ends, wherein both ends comprise a nucleotide overhang of 1 to 4 unpaired nucleotides in length;
- (b) selecting a dsRNA comprising first and second double-stranded ends, wherein the nucleotide overhang on at least one end is 5'-GC-3';
- (c) selecting a dsRNA comprising first and second double stranded ends, wherein the terminal base pair of the first double-stranded end comprises a guanine-cytosine (G-C) base pair or the four consecutive terminal base pairs of the first double-stranded end comprises at least two G-C base pairs; wherein the terminal base pair of the second double-stranded end comprises a guanine-cytosine (G-C) base pair or the four consecutive terminal base pairs of the second double-stranded end comprises at least two G-C base pairs; and
- (d) excluding the following dsRNAs:

5'- CCGCUUGACUGCAGAGAGUGC-3' (SEQ ID NO: 19)
 3'-UCGGCGAACUGACGUCUCUCA-5' (SEQ ID NO: 20),

5'- CAUCUUCUUCAAGGACGACGGC-3' (SEQ ID NO: 21)
 3'-UGGUAGAAGAAGUUCCUGCUGC-5' (SEQ ID NO: 22),

 5'- GGUGGCGCUGGAUGGUAAGCCGC-3' (SEQ ID NO: 23)
 3'-UACCACCGCGACCUACCAUUCGG-5' (SEQ ID NO: 24),

 5'- UCCCCAGGAGGCCUGCGGGAGC-3' (SEQ ID NO: 25)
 3'-GGAGGGGUCCUCCGGACGCCCU-5' (SEQ ID NO: 26),

 5'- UGCAGCUUCGAAGCCUCACAGA-3' (SEQ ID NO: 27)
 3'-CGACGUCGAAGCUUCGGAGUGU-5' (SEQ ID NO: 28),

 5'- UGGGGAGAGAGUUCUGAGGAUU-3' (SEQ ID NO: 29)
 3'-CGACCCUCUCUCAAGACUCCU-5' (SEQ ID NO: 30),

 5'- ACCUCCGCAACAACUACGCGC-3' (SEQ ID NO: 31)
 3'-GAUGGAGGCGUUGUUGAUGCG-5' (SEQ ID NO: 32),

 5'- GUAGACCUUGCUCUACUGCCUGC-3' (SEQ ID NO: 33)
 3'-ACCAUCUGGAACGAUGACGGA-5' (SEQ ID NO: 34),

 5'- CAUGACGGAACUAGAGACAGC-3' (SEQ ID NO: 35)
 3'-UGGUACUGCCUUGAUCUCUGU-5' (SEQ ID NO: 36),

 5'- CUCUACGCUUGUACGAGGAGC-3' (SEQ ID NO: 37)
 3'-CAGAGAUGCGAACAUGCUCU-5' (SEQ ID NO: 38),

 5'- CAGACUUCGGAGUACCUGCGC-3' (SEQ ID NO: 39)
 3'-UUGUCUGAAGCCUCAUGGACG-5' (SEQ ID NO: 40) and

 5'- CAUCUUCUUCAAGGACGACGGC-3' (SEQ ID NO: 41)
 3'-UGGUAGAAGAAGUUCCUGCUGC-5' (SEQ ID NO: 42).

21. **(original)** The method of claim 19 or 20, wherein each nucleotide overhang independently consists of 1 or 2 unpaired nucleotides.

22. **(original)** The methods of claim 19 or 20, wherein at least half of the unpaired nucleotides comprise a purine base.

23. **(original)** The method of claim 19, wherein the unpaired nucleotide adjacent to the terminal nucleotide base pair comprises a guanine (G) base.
24. **(original)** The method of claim 19, wherein the unpaired nucleotide adjacent to the terminal nucleotide base pair comprises an adenine (A) base.
25. **(original)** The method of claim 19, wherein the nucleotide overhang consists of the sequence 5'-GC-3'.
26. **(original)** The method of claim 20, wherein the unpaired nucleotide adjacent to the terminal nucleotide base pair comprise a guanine (G) base.
27. **(original)** The method of claim 20, wherein the unpaired nucleotide adjacent to the terminal nucleotide base pair comprise an adenine (A) base.
28. **(original)** The method of claim 19 or 20, wherein the first single RNA strand is an antisense RNA strand, the second single RNA strand is a sense RNA strand, wherein the antisense RNA strand is complementary to a target gene or a portion thereof.
29. **(currently amended)** The method of claim 28, wherein ~~the~~ a nucleotide overhang is at the 3' end of the antisense strand.
30. **(original)** The method of claim 28, wherein the region of the antisense strand that is complementary to the target gene is 19 to 24 nucleotides in length.
31. **(original)** The method of claim 28, wherein the antisense strand is 20 to 28 nucleotides in length.
32. **(original)** The method of claim 28, wherein the antisense strand is 21 nucleotides in length.
33. **(original)** The method of claim 19 or 20, comprising at least one chemically modified nucleotide.
34. **(original)** The method of claim 33, wherein the chemically modified nucleotide comprises a non-natural base.
35. **(original)** The methods of claim 33, wherein the chemically modified nucleotide comprises a 2' modification.

36. **(original)** The method of claim 35, wherein the 2' modification is selected from the group consisting of a 2'-amino modification, a 2'-alkyl modification, and a 2'-O-methyl modification, a 2'-O-ethyl modification, a 2'-O-propyl modification, a 2'-O-allyl modification, a 2'-O-aminoalkyl modification, and a 2'-deoxy-2'-fluoro modification.

37. **(canceled)**

38. **(currently amended)** A method for inhibiting the expression of a target gene in a cell, comprising:

(a) introducing into the cell a dsRNA of [[any one of claims 1-18]] claim 2, or a salt, prodrug or hydrate thereof; and

(b) maintaining the cell for a time sufficient to obtain degradation of a mRNA transcript of the target gene.

Claims 39-43 **(canceled)**